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Sequence Listing was accepted with existing errors.

See attached Validation Report.

If you need help call the Patent Electronic Business Center at (866)  
217-9197 (toll free).

Reviewer: Anne Corrigan

Timestamp: Wed Jul 25 18:16:00 EDT 2007

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Application No: 10590810

Version No: 1.1

Input Set:

Output Set:

Started: 2007-07-25 18:15:36.750

Finished: 2007-07-25 18:15:42.305

Elapsed: 0 hr(s) 0 min(s) 5 sec(s) 555 ms

Total Warnings: 36

Total Errors: 2

No. of SeqIDs Defined: 108

Actual SeqID Count: 108

Error code	Error Description
W 213	Artificial or Unknown found in <213> in SEQ ID (1)
W 213	Artificial or Unknown found in <213> in SEQ ID (2)
W 213	Artificial or Unknown found in <213> in SEQ ID (3)
W 213	Artificial or Unknown found in <213> in SEQ ID (4)
W 213	Artificial or Unknown found in <213> in SEQ ID (5)
W 213	Artificial or Unknown found in <213> in SEQ ID (6)
W 213	Artificial or Unknown found in <213> in SEQ ID (7)
W 213	Artificial or Unknown found in <213> in SEQ ID (8)
W 213	Artificial or Unknown found in <213> in SEQ ID (9)
W 213	Artificial or Unknown found in <213> in SEQ ID (10)
W 213	Artificial or Unknown found in <213> in SEQ ID (11)
W 213	Artificial or Unknown found in <213> in SEQ ID (12)
W 213	Artificial or Unknown found in <213> in SEQ ID (13)
W 213	Artificial or Unknown found in <213> in SEQ ID (14)
W 213	Artificial or Unknown found in <213> in SEQ ID (15)
W 213	Artificial or Unknown found in <213> in SEQ ID (16)
W 213	Artificial or Unknown found in <213> in SEQ ID (17)
W 213	Artificial or Unknown found in <213> in SEQ ID (18)
E 355	Empty lines found between the amino acid numbering and the
E 321	No. of Bases conflict, this line has no nucleotides SEQID (34)

**Input Set:**

**Output Set:**

**Started:** 2007-07-25 18:15:36.750  
**Finished:** 2007-07-25 18:15:42.305  
**Elapsed:** 0 hr(s) 0 min(s) 5 sec(s) 555 ms  
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**No. of SeqIDs Defined:** 108  
**Actual SeqID Count:** 108

Error code	Error Description
W 213	Artificial or Unknown found in <213> in SEQ ID (39)
W 213	Artificial or Unknown found in <213> in SEQ ID (40) This error has occurred more than 20 times, will not be displayed

SUBSTITUTE SEQUENCE LISTING

<110> JESTIN, JEAN-LUC  
VICHIER-GUERRE, SOPHIE  
FERRIS, STEPHANE

<120> METHODS FOR OBTAINING THERMOSTABLE ENZYMES, DNA POLYMERASE I  
VARIANTS FROM THERMUS AQUATICUS HAVING NEW CATALYTIC ACTIVITIES,  
METHODS FOR OBTAINING THE SAME, AND APPLICATIONS OF THE SAME

<130> 295295US-10590810

<140> 10/590,810

<141> 2006-08-25

<150> PCT/IB05/00734

<151> 2005-02-25

<150> 10/787,219

<151> 2004-02-27

<160> 108

<170> PatentIn version 3.3

<210> 1

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic oligonucleotide

<400> 1

taacaatagg ccggccaccc cttc

24

<210> 2

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic oligonucleotide

<400> 2

gagtttttgt tctgcggc

18

<210> 3

<211> 27

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic oligonucleotide

<400> 3  
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<210> 4  
 <211> 28  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic oligonucleotide

<400> 4  
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<210> 5  
 <211> 43  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic oligonucleotide

<220>  
 <221> modified\_base  
 <222> (15)..(17)  
 <223> This region may encompass the bases "car" or "avy"

<220>  
 <221> modified\_base  
 <222> (24)..(26)  
 <223> This region may encompass the bases "car" or "avy"

<400> 5  
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<210> 6  
 <211> 65  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic oligonucleotide

<220>  
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 <223> This region may encompass the bases "ytg" or "rbt"

<220>  
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 <222> (20)..(22)  
 <223> This region may encompass the bases "ytg" or "rbt"

<220>

<221> modified\_base  
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 <223> This region may encompass the bases "ytg" or "rbt"

<220>  
 <221> modified\_base  
 <222> (44)..(46)  
 <223> This region may encompass the bases "ytg" or "rbt"

<400> 6  
 ggatgaggtc cggcaannnn nnaatnnngg tgctcttcag cttnnngagc tcccgggtact 60  
 gcagg 65

<210> 7  
 <211> 62  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic oligonucleotide

<220>  
 <221> modified\_base  
 <222> (17)..(19)  
 <223> This region may encompass the bases "car" or "avy"

<220>  
 <221> modified\_base  
 <222> (32)..(34)  
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<220>  
 <221> modified\_base  
 <222> (41)..(43)  
 <223> This region may encompass the bases "car" or "avy"

<400> 7  
 caaccagacg gccacgnnna cgggcaggct annnagctcc nnncccaacc tccagaacat 60  
 cc 62

<210> 8  
 <211> 43  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic oligonucleotide

<220>  
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 <222> (14)..(16)  
 <223> This region may encompass the bases "ytg" or "rbt"

<220>  
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 <222> (23)..(25)  
 <223> This region may encompass the bases "ytg" or "rbt"  
  
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 ccgctctcccg cacnnncttc acnnnggcct ctaggtctgg cac 43  
  
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 <213> Artificial Sequence  
  
 <220>  
 <223> Description of Artificial Sequence: Synthetic oligonucleotide  
  
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 <222> (20)..(22)  
 <223> This region may encompass the bases "car" or "avy"  
  
 <220>  
 <221> modified\_base  
 <222> (38)..(40)  
 <223> This region may encompass the bases "car" or "avy"  
  
 <220>  
 <221> modified\_base  
 <222> (44)..(46)  
 <223> This region may encompass the bases "car" or "avy"  
  
 <220>  
 <221> modified\_base  
 <222> (47)..(49)  
 <223> This region may encompass the bases "car" or "avy"  
  
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 cctgcagtac cgggagctcn nnaagctgaa gagcaccnnn attnnnnnnt tgccggacct 60  
  
 catcc 65  
  
 <210> 10  
 <211> 62  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Description of Artificial Sequence: Synthetic oligonucleotide  
  
 <220>  
 <221> modified\_base  
 <222> (20)..(22)  
 <223> This region may encompass the bases "ytg" or "rbt"  
  
 <220>

<221> modified\_base  
 <222> (29)..(31)  
 <223> This region may encompass the bases "ytg" or "rbt"  
  
 <220>  
 <221> modified\_base  
 <222> (44)..(46)  
 <223> This region may encompass the bases "ytg" or "rbt"  
  
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 tg 62  
  
 <210> 11  
 <211> 43  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Description of Artificial Sequence: Synthetic oligonucleotide  
  
 <220>  
 <221> modified\_base  
 <222> (19)..(21)  
 <223> This region may encompass the bases "car" or "avy"  
  
 <220>  
 <221> modified\_base  
 <222> (28)..(30)  
 <223> n is a, c, g, or t  
  
 <220>  
 <221> modified\_base  
 <222> (28)..(30)  
 <223> This region may encompass the bases "car" or "avy"  
  
 <400> 11  
 gtgccagacc tagaggccnn ngtgaagnnn gtgcgggagg cgg 43  
  
 <210> 12  
 <211> 30  
 <212> RNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Description of Artificial Sequence: Synthetic oligonucleotide  
  
 <400> 12  
 aaauacaaca auaaaacgcc acaucuugcg 30  
  
 <210> 13  
 <211> 28  
 <212> DNA



<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic oligonucleotide

<400> 13

taacacgaca aagcgcaaga tgtggcgt 28

<210> 14

<211> 30

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic oligonucleotide

<400> 14

aaatacaaca ataaaacgcc acatcttgcg 30

<210> 15

<211> 28

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic oligonucleotide

<400> 15

ttcattcttg ctagctcctg ggagaggc 28

<210> 16

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic oligonucleotide

<400> 16

gagaagatcc tgcagtaccg ggagc 25

<210> 17

<211> 19

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic oligonucleotide

<400> 17

gaccaacatc aagactgcc 19

<210> 18  
 <211> 18  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Description of Artificial Sequence: Synthetic oligonucleotide  
  
 <400> 18  
 ttggccagga acttgccc 18  
  
  
 <210> 19  
 <211> 1688  
 <212> DNA  
 <213> Thermus aquaticus  
  
 <220>  
 <221> CDS  
 <222> (3)..(1688)  
  
 <400> 19  
 cc atg gcc tct ggt ggc ggt ggc tgt ggt ggc ggt ggc agc ccc aag 47  
 Met Ala Ser Gly Gly Gly Cys Gly Gly Gly Gly Ser Pro Lys  
 1 5 10 15  
  
 gcc ctg gag gag gcc ccc tgg ccc ccg ccg gaa ggg gcc ttc gtg ggc 95  
 Ala Leu Glu Glu Ala Pro Trp Pro Pro Pro Glu Gly Ala Phe Val Gly  
 20 25 30  
  
 ttt gtg ctt tcc cgc aag gag ccc atg tgg gcc gat ctt ctg gcc ctg 143  
 Phe Val Leu Ser Arg Lys Glu Pro Met Trp Ala Asp Leu Leu Ala Leu  
 35 40 45  
  
 gcc gcc gcc agg ggg ggc cgg gtc cac cgg gcc ccc gag cct tat aaa 191  
 Ala Ala Ala Arg Gly Gly Arg Val His Arg Ala Pro Glu Pro Tyr Lys  
 50 55 60  
  
 gcc ctc agg gac ctg aag gag gcg cgg ggg ctt ctc gcc aaa gac ctg 239  
 Ala Leu Arg Asp Leu Lys Glu Ala Arg Gly Leu Leu Ala Lys Asp Leu  
 65 70 75  
  
 agc gtt ctg gcc ctg agg gaa ggc ctt ggc ctc ccg ccc ggc gac gac 287  
 Ser Val Leu Ala Leu Arg Glu Gly Leu Gly Leu Pro Pro Gly Asp Asp  
 80 85 90 95  
  
 ccc atg ctc ctc gcc tac ctc ctg gac cct tcc aac acc acc ccc gag 335  
 Pro Met Leu Leu Ala Tyr Leu Leu Asp Pro Ser Asn Thr Thr Pro Glu  
 100 105 110  
  
 ggg gtg gcc cgg cgc tac ggc ggg gag tgg acg gag gag gcg ggg gag 383  
 Gly Val Ala Arg Arg Tyr Gly Gly Glu Trp Thr Glu Glu Ala Gly Glu  
 115 120 125  
  
 cgg gcc gcc ctt tcc gag agg ctc ttc gcc aac ctg tgg ggg agg ctt 431  
 Arg Ala Ala Leu Ser Glu Arg Leu Phe Ala Asn Leu Trp Gly Arg Leu  
 130 135 140

gag ggg gag gag agg ctc ctt tgg ctt tac cgg gag gtg gag agg ccc	479
Glu Gly Glu Glu Arg Leu Leu Trp Leu Tyr Arg Glu Val Glu Arg Pro	
145 150 155	
ctt tcc gct gtc ctg gcc cac atg gag gcc acg ggg gtg cgc ctg gac	527
Leu Ser Ala Val Leu Ala His Met Glu Ala Thr Gly Val Arg Leu Asp	
160 165 170 175	
gtg gcc tat ctc agg gcc ttg tcc ctg gag gtg gcc gag gag atc gcc	575
Val Ala Tyr Leu Arg Ala Leu Ser Leu Glu Val Ala Glu Glu Ile Ala	
180 185 190	
cgc ctc gag gcc gag gtc ttc cgc ctg gcc ggc cac ccc ttc aac ctc	623
Arg Leu Glu Ala Glu Val Phe Arg Leu Ala Gly His Pro Phe Asn Leu	
195 200 205	
aac tcc cgg gac cag ctg gaa agg gtc ctc ttt gac gag cta ggg ctt	671
Asn Ser Arg Asp Gln Leu Glu Arg Val Leu Phe Asp Glu Leu Gly Leu	
210 215 220	
ccc gcc atc ggc aag acg gag aag acc ggc aag cgc tcc acc agc gcc	719
Pro Ala Ile Gly Lys Thr Glu Lys Thr Gly Lys Arg Ser Thr Ser Ala	
225 230 235	
gcc gtc ctg gag gcc ctt cgc gag gcc cac ccc atc gtg gag aag atc	767
Ala Val Leu Glu Ala Leu Arg Glu Ala His Pro Ile Val Glu Lys Ile	
240 245 250 255	
ctg cag tac cgg gag ctc acc aag ctg aag agc acc tac att ggc ccc	815
Leu Gln Tyr Arg Glu Leu Thr Lys Leu Lys Ser Thr Tyr Ile Gly Pro	
260 265 270	
ttg ccg gac ctc atc cac ccc agg acg ggc cgc ctc cac acc cgc ttc	863
Leu Pro Asp Leu Ile His Pro Arg Thr Gly Arg Leu His Thr Arg Phe	
275 280 285	
aac cag acg gcc acg gcc acg ggc agg cta agt agc tcc gat ccc aac	911
Asn Gln Thr Ala Thr Ala Thr Gly Arg Leu Ser Ser Ser Asp Pro Asn	
290 295 300	
ctc cag aac gtc ccc gtc cgc acc ccg ctt ggg cag agg atc cgc cgg	959
Leu Gln Asn Val Pro Val Arg Thr Pro Leu Gly Gln Arg Ile Arg Arg	
305 310 315	
gcc ttc atc gcc gag gag ggg tgg cta ttg gtg gcc ctg gac tat agc	1007
Ala Phe Ile Ala Glu Glu Gly Trp Leu Leu Val Ala Leu Asp Tyr Ser	
320 325 330 335	
cag ata gag ctc agg gtg ctg gcc cac ctc tcc ggc gac gag aac ctg	1055
Gln Ile Glu Leu Arg Val Leu Ala His Leu Ser Gly Asp Glu Asn Leu	
340 345 350	
atc cgg gtc ttc cag gag ggg cgg gat atc cac acg gag acc gcc agc	1103
Ile Arg Val Phe Gln Glu Gly Arg Asp Ile His Thr Glu Thr Ala Ser	
355 360 365	

tgg atg ttc ggc gtc ccc cgg gag gcc gtg gac ccc ctg atg cgc cgg	1151
Trp Met Phe Gly Val Pro Arg Glu Ala Val Asp Pro Leu Met Arg Arg	
370 375 380	
gcg gcc aag acc atc aac ttc ggg gtc ctc tac ggc atg tcg gcc cac	1199
Ala Ala Lys Thr Ile Asn Phe Gly Val Leu Tyr Gly Met Ser Ala His	
385 390 395	
cgc ctc tcc cag gag cta gcc atc cct tac gag gag gcc cag gcc ttc	1247
Arg Leu Ser Gln Glu Leu Ala Ile Pro Tyr Glu Glu Ala Gln Ala Phe	
400 405 410 415	
att gag cgc tac ttt cag agc ttc ccc aag gtg cgg gcc tgg att gag	1295
Ile Glu Arg Tyr Phe Gln Ser Phe Pro Lys Val Arg Ala Trp Ile Glu	
420 425 430	
aag acc ctg gag gag ggt agg agg cgg ggg tac gtg gag acc ctc ttc	1343
Lys Thr Leu Glu Glu Gly Arg Arg Arg Gly Tyr Val Glu Thr Leu Phe	
435 440 445	
ggc cgc cgc cgc tac gtg cca gac cta gag gcc cgg gtg aag agc gtg	1391
Gly Arg Arg Arg Tyr Val Pro Asp Leu Glu Ala Arg Val Lys Ser Val	
450 455 460	
cgg gag gcg gcc gag cgc atg gcc ttc aac atg ccc gtc cag ggc acc	1439
Arg Glu Ala Ala Glu Arg Met Ala Phe Asn Met Pro Val Gln Gly Thr	
465 470 475	
gcc gcc gac ctc acg aag ctg gct atg gtg aag ctc ttc ccc agg ctg	1487
Ala Ala Asp Leu Thr Lys Leu Ala Met Val Lys Leu Phe Pro Arg Leu	
480 485 490 495	
gag gaa atg ggg gcc agg atg ctc ctt cag gtc cac gac gag ctg gtc	1535
Glu Glu Met Gly Ala Arg Met Leu Leu Gln Val His Asp Glu Leu Val	
500 505 510	
ctc gag gcc cca aaa gag ggg gcg gag gcc gtg gcc cgg ctg gcc aag	1583
Leu Glu Ala Pro Lys Glu Gly Ala Glu Ala Val Ala Arg Leu Ala Lys	
515 520 525	
gag gtc atg gag ggg gtg tat ccc ctg gcc gtg ccc ctg gag gtg gag	1631
Glu Val Met Glu Gly Val Tyr Pro Leu Ala Val Pro Leu Glu Val Glu	
530 535 540	
gtg ggg ata ggg gag gac tgg ctc tcc gcc aag gag gcg gcc gca ctg	1679
Val Gly Ile Gly Glu Asp Trp Leu Ser Ala Lys Glu Ala Ala Ala Leu	
545 550 555	
gtg ccg cgc	1688
Val Pro Arg	
560	

<210> 20

<211> 562

<212> PRT

<213> Thermus aquaticus

<400> 20

Met Ala Ser Gly Gly Gly Gly Cys Gly Gly Gly Gly Ser Pro Lys Ala  
1 5 10 15

Leu Glu Glu Ala Pro Trp Pro Pro Pro Glu Gly Ala Phe Val Gly Phe  
20 25 30

Val Leu Ser Arg Lys Glu Pro Met Trp Ala Asp Leu Leu Ala Leu Ala  
35 40 45

Ala Ala Arg Gly Gly Arg Val His Arg Ala Pro Glu Pro Tyr Lys Ala  
50 55 60

Leu Arg Asp Leu Lys Glu Ala Arg Gly Leu Leu Ala Lys Asp Leu Ser  
65 70 75 80

Val Leu Ala Leu Arg Glu Gly Leu Gly Leu Pro Pro Gly Asp Asp Pro  
85 90 95

Met Leu Leu Ala Tyr Leu Leu Asp Pro Ser Asn Thr Thr Pro Glu Gly  
100 105 110

Val Ala Arg Arg Tyr Gly Gly Glu Trp Thr Glu Glu Ala Gly Glu Arg  
115 120 125

Ala Ala Leu Ser Glu Arg Leu Phe Ala Asn Leu Trp Gly Arg Leu Glu  
130 135 140

Gly Glu Glu Arg Leu Leu Trp Leu Tyr Arg Glu Val Glu Arg Pro Leu  
145 150 155 160

Ser Ala Val Leu Ala His Met Glu Ala Thr Gly Val Arg Leu Asp Val  
165 170 175

Ala Tyr Leu Arg Ala Leu Ser Leu Glu Val Ala Glu Glu Ile Ala Arg  
180 185 190

Leu Glu Ala Glu Val Phe Arg Leu Ala Gly His Pro Phe Asn Leu Asn  
195 200 205

Ser Arg Asp Gln Leu Glu Arg Val Leu Phe Asp Glu Leu Gly Leu Pro  
210 215 220

Ala Ile Gly Lys Thr Glu Lys Thr Gly Lys Arg Ser Thr Ser Ala Ala  
225 230 235 240

Val Leu Glu Ala Leu Arg Glu Ala His Pro Ile Val Glu Lys Ile Leu  
245 250 255

Gln Tyr Arg Glu Leu Thr Lys Leu Lys Ser Thr Tyr Ile Gly Pro Leu  
260 265 270

Pro Asp Leu Ile His Pro Arg Thr Gly Arg Leu His Thr Arg Phe Asn  
275 280 285

Gln Thr Ala Thr Ala Thr Gly Arg Leu Ser Ser Ser Asp Pro Asn Leu  
290 295 300

Gln Asn Val Pro Val Arg Thr Pro Le